

FIG. 4

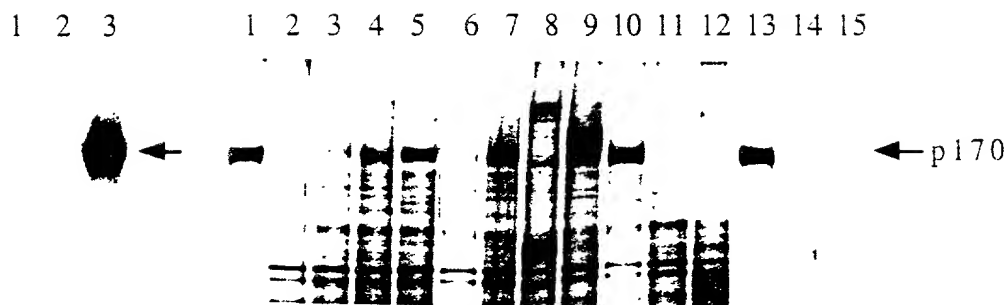


FIG. 5A

FIG. 5B

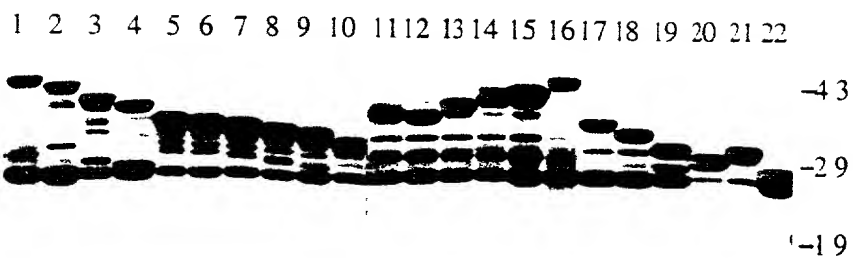


FIG. 7A

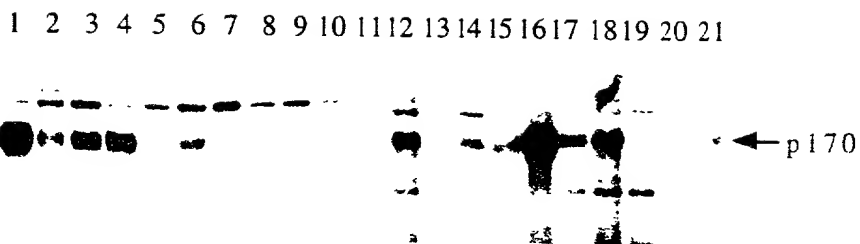


FIG. 7B

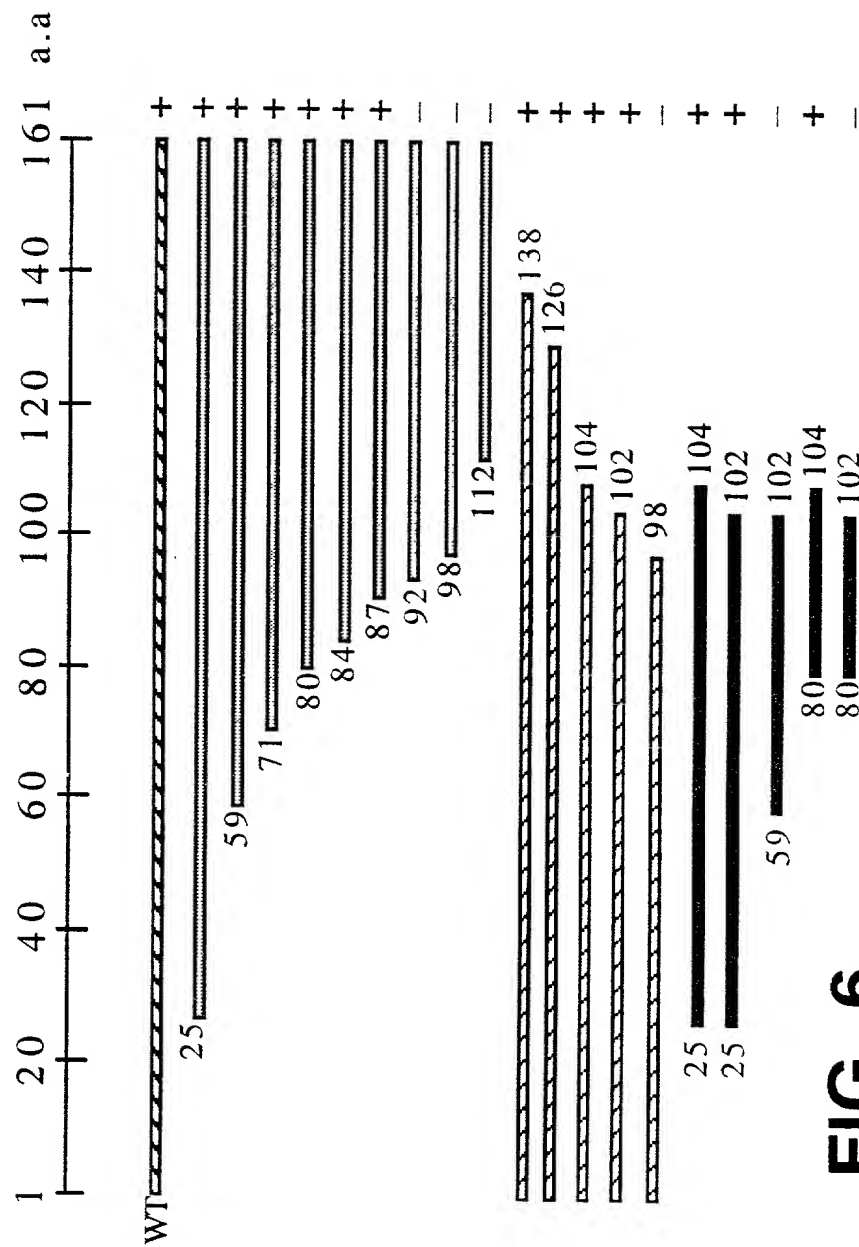
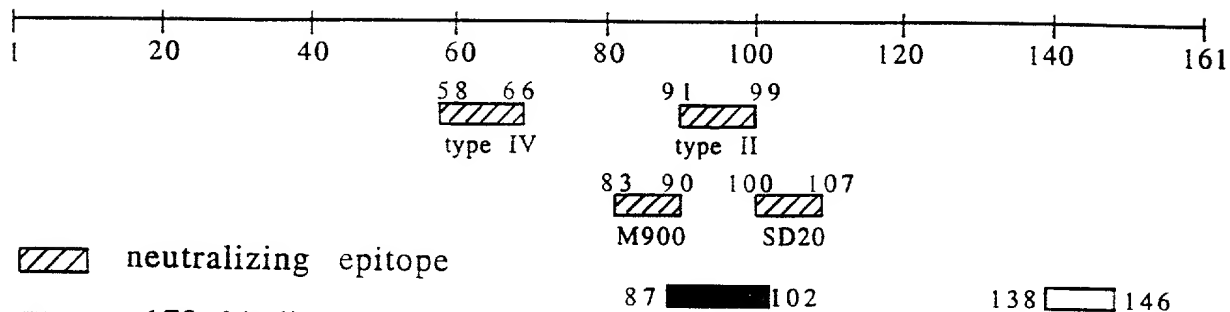


FIG. 6

DHBV pre-S region



neutralizing epitope

p170 binding site

non-essential space

FIG. 8

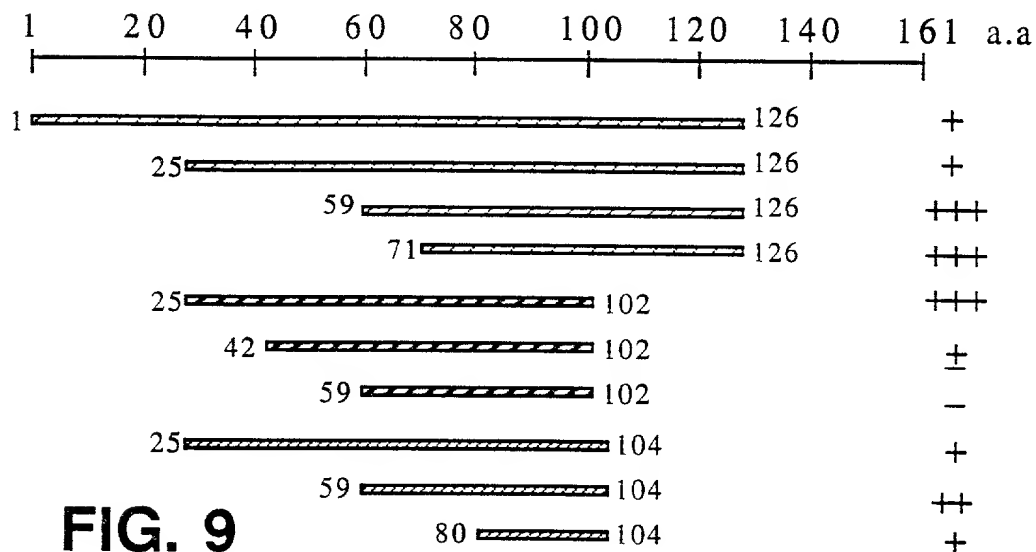


FIG. 9

1 2 3 4 5 6 7 8 9 10 11



FIG. 10

A pre-S polypeptide containing p170 binding site blocks DHBV infectivity

1 2 3 4



FIG. 11

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16

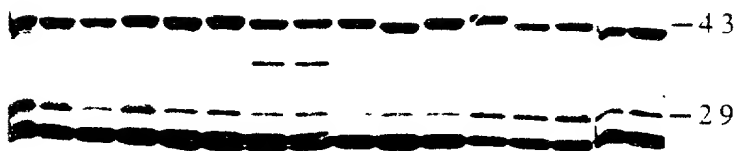


FIG. 13A

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18



FIG. 13B

	87	90	93	96	99	102										
wild-type	Q	W	T	P	E	E	D	Q	K	A	R	E	<u>A</u>	F	R	R
W88S		S														
P90L			L													
E91G				G												
E92V					V											
D93F						F										
K95S								S								
R97L											L					
R97C											C					
E98A												A				
E98V												V				
R102G															G	
E91G/K95S				G				S								
E91G/R97C				G							C					
K95S/A96T								S	T							
K95S/R97C								S			C					
K95S/R97L/E98A								S			L	A				

FIG. 12

peptide 1	SVELRELYVMEISDNPGVHEAGEPEFK (SEQ ID NO:19)
peptide 2	LIDRTRIVIVPSLNPDGR-IA (SEQ ID NO:20)
peptide 3	SLLSHEFQDETDTTEEETLYSAK (SEQ ID NO:21)
peptide 4	VEEGKVPVLNTPD (SEQ ID NO:22)

FIG. 14A

peptide 1	SVELRELYVMEISDNPGVHEAGEPEFK (SEQ ID NO:19)
bovine CPH	.F.G...L.L.L.....P.....
human CPH	.F.G...L.I.L.....P.....
AEBP1 gene	KI.A.....D..L.....R
human CPN	...G.H...L.F..H..I..PL...V.
human CPM	..KG.N.W.LVVGRF.KE.RI.I....

peptide 2	LIDRTRIVIVPSLNPDGR-IA (SEQ ID NO:20)
AEBP1 gene	.VQD...HL.....YEV.
bovine CPH	..HN...H.M.....
human CPN	..QD...H.L..M....YEV.
human CPM	..NS...H.M..M....
human CPH	..HS...H.M.....

FIG. 14B

		(SEQ ID NO:)	
PK-81			
aa number	6	7	8
aa	E	L	Y
possible nt	GAX CTN TAY	GTN ATG GAX ATW AGY	AGY GAY AAY CCN GGN GTN CAY GAX GCN GGN GAX CCN GAX TTY AAX
degenerate primer & product	gax ytn tay	atg gag atc	gag atc TCG GAC AAC CCC GGY GTY cay gax gcg ggn gax ccn gax tt
specific primer & product	atg gag atc	tcg gag aac ccc GGC GTC CAT GAA GCA GGT GAG CCA GAG TTC AAG	
PK-69			
aa number	1	2	3
aa	S	L	L
possible nt	AGY CTN CTN AGY CAY GAX TTY CAX	GAY GAX ACN GAY ACN GAY GAX GAT GAA ACA GAC ACT GAA GAA gax acn ytn tay tcg gcv aa	TCN TTX TTX TCN
degenerate primer & product	tz ytn agy cay gax tty cax	tcg gag aac ccc GGC GTC CAT GAA GCA GGT GAG CCA GAG TTC AAG	
specific primer & product	TCC CTT TTG AGC CAC GAA TTC CAG	Gat gaa aca gac act gaa gaa	

N: G/A/T/C; X: A/G; Y: C/T; Z: G/T; V: A/C; W: A/T/C.

Primer sequences are written in small letters. For convenience antisense primers are written in the sense orientation.

FIG. 15

1/1	ATG GGG CAA CAT CCA GCA AAA TCA ATG GAC GTC AGA CGG ATA GAA GGA GGA GAA ATA CTG	(SEQ ID NO:33)
M G	Q Q H P A K S M D V R	(SEQ ID NO:34)
61/21	TTA AAC CAA CTT GCC GGA AGG ATG ATC CCA AAA GGG ACT TTG ACA TGG TCA GGC AAG TTT	
L N	Q Q L A G R M I P K G T L T W S G K F	
121/41	CCA ACA CTA GAT CAC GTG TTA GAC CAT GTG CAA ACA ATG GAG GAG ATA AAC ACC CTC CAG	
P T	L D H V L D H V Q T M E I N T L Q	
181/61	AAT CAG GGA GCT TGG CCT GCT GGG GCG GGA AGG AGA GTA GGA TTA TCA AAT CCG ACT CCT	
N Q	G A W P A G A G R R V G L S N P T P	
241/81	CAA GAG ATT CCT CAG CCC CAG TGG ACT CCC GAG GAA GAC CAA AAA GCA CGC GAA GCT TTT	
Q E	I P Q P Q W T P E E D Q K A R E A F	
301/101	CGC CGT TAT CAA GAA GAA AGA CCA CCG GAA ACC ACC ACC ATT CCT CCG TCT TCC CCT CCT	
R R	Y Q E E R P P E T T I P P S S P P	
361/121	CAG TGG AAG CTA CAA CCC GGG GAC GAT CCA CTC CTG GGA AAT CAG TCT CTC CTC GAG ACT	
Q W	K L Q P G D D P L L L G N Q S L L E T	
421/141	CAT CCG CTA TAC CAG TCA GAA CCA CCG GTG CCA GTG ATA AAA ACT CCC CCC TTG AAG AAG	
H P	L Y Q S E P A V I K T P P L K K	
481/161	AAA	
	K	

FIG. 16

FIG. 17A

FIG. 17B

FIG. 17C

FIG. 17D

FIG. 17E

FIG. 17

[illegible]

FIG. 17A

(SEQ ID NO:)

119
 (35)
 (36)
 (37)
 (38)
 (39)
 (40)
 (41)
 (42)
 (43)
 (44)
 (45)
 (46)
 (47)
 (48)
 (49)
 (50)
 (51)
 (52)
 (53)
 (54)
 (55)
 (56)
 (57)
 (58)
 (59)
 (60)
 (61)
 (62)

FIG. 17B

[illegible]

FIG. 17E

1/1
 ATG GAG ATC TCG GAC AAC CCC GGT GTT CAT GAA GCA GGT GAG CCA GAG TTC AAG TAT ATT
 M E I S D N P G V H E A G E P E F K Y I

61/21
 GGT AAC ATG CAT GGG AAT GAA GTT GTG GGG CGA GAG CTG CTC CTG AAC CTC ATC GAG TAC
 G N M H G N E V V G R E L L L N L I E Y

121/41
 CTC TGC AAG AAC TTC GGC ACA GAT CCC GAA GTG ACT GAC TTG GTC CAG AGC ACG CGG ATC
 L C K N F G T D P E V T D L V Q S T R I

181/61
 CAC ATC ATG CCG TCC ATG AAC CCA GAT GGC TAC GAG AAG TCC CAG GAA GGA GAC AGA GGA
 H I M P S M N P D G Y E K S Q E G D R G

241/81
 GGC ACC GTT GGC AGA AAT AAC AGC AAC AAC TAC GAC CTG AAC CGG AAC TTC CCA GAT CAG
 G T V G R N N S N N Y D L N R N F P D Q

301/101
 TTC TTC CAG GTG ACA GAC CCT CCG CAG CCA GAA ACT CTT GCT GTC ATG AGC TGG TTG AAA
 F F Q V T D P P Q P E T L A V M S W L K

361/121
 ACT TAC CCG TTC GTG CTT TCA GCA AAC CTG CAT GGA GGT TCT CTG GTG GTT AAT TAC CCT
 T Y P F V L S A N L H G G S L V V N Y P

421/141
 TTT GAT GAC GAT GAA CAA GGA ATA GCC ATA TAC AGT AAA TCC CCA GAC GAT GCT GTG TTT
 F D D D E Q G I A I Y S K S P D D A V F

481/161
 CAG CAG CTG GCA CTT TCC TAC TCC AAG GAA AAC AAA AAG ATG TAT CAG GGA AGC CCT TGT
 Q Q L A L S Y S K E N K K M Y Q G S P C

541/181
 AAG GAT TTG TAC CCC ACA GAG TAC TTT CCA CAT GGC ATC ACG AAC GGG GCC CAG TGG TAC
 K D L Y P T E Y F P H G I T N G A Q W Y

601/201
 AAC GTT CCA GGT GGG ATG CAG GAC TGG AAT TAC TTA AAT ACC AAC CTG TTT GAA GTG ACC
 N V P G G M Q D W N Y L N T N L F E V T

661/221
 ATT GAG CTG GGC TGT GTG AAA TAC CCA AAA GCA GAG GAG CTG CCG AAG TAC TGG GAG CAG
 I E L G C V K Y P K A E E L P K Y W E Q

721/241
 AAC CGT AGA TCT CTC CTC CAG TTC ATT AAA CAG GTT CAC CGC GGC ATC TGG GGA TTT GTG
 N R R S L L Q F I K Q V H R G I W G F V

781/261
 CTG GAT GCC ACG GAC GGA AGG GGC ATT CTC AAC GCC ACC ATC AGC GTC GCC GAC ATC AAC
 L D A T D G R G I L N A T I S V A D I N

841/281
 CAC CCC GTG ACC ACC TAC AAA GAT GGG GAC TAC TGG CGC CTC TTG GTC CAG GGG ACG TAC
 H P V T T Y K D G D Y W R L L V Q G T Y

901/301
 AAA GTC ACA GCA TCT GCC CGA GGG TAT GAT CCA GTC ACT AAA ACG GTG GAA GTC GAC AGC
 K V T A S A R G Y D P V T K T V E V D S

961/321
 AAA GGT GGG GTG CAG GTC AAC TTC ACT CTT TCA CGG ACA GAC GCC AAA GTG GAG GAG GGG
 K G G V Q V N F T L S R T D A K V E E G

1021/341
 AAG GTG CCA GTC CTG AAC ACC CCA GAC ACC AGC GAC CCC AAC GAG AAG GAG TTT GAG ACT
 K V P V L N T P D T S D P N E K E F E T

1081/361
 CTG ATC AAA GAT CTA TCT GCT GAA AAC GGC CTG GAG (SEQ ID NO:63)
 L I K D L S A E N G L E (SEQ ID NO:64)

FIG. 18

1/1
 TTT GTC CAG GAC AAG AGT GGC AAG GCA ATT TCT AAA GCT ACC ATT GTC CTT AAT GAA GGC
 F V Q D K S G K A I S K A T I V L N E G
 61/21
 TTG AGG GTC TAC ACT AAA GAA GGT GGC TAT TTC CAT GTG CTG TTG GCT CCT GGT TTG CAT
 L R V Y T K E G G Y F H V L A P G L H
 121/41
 AAC ATC AAT GCG ATA GCG GAT GGG TAC CAA CAA AAG CAT ATG AAG GTC TTG GTA CGC CAC
 N I N A I A D G Y Q Q K H M K V L V R H
 181/61
 GAT GCA CCC AGC TCT GTG TTC ATG GTA TTT GAC ATG GAA AAC AGG ATA TTT GGT CTG CCT
 D A P S S V F M V F D M E N R I F G L P
 241/81
 CGA GAG CTG GTT GTA ACT GTT GCA GGT GCA ATT ATG TCT GCT TTG GTC CTC ACT GCC TGT
 R E L V V T V A G A I M S A L V L T A C
 301/101
 ATC ATC TGG TGT GTC TGC TCA ATC AAG GCC AAC AGA CAC AAA GAT GGC TTC CAC TGC CGG
 I I W C V C S I K A N R H K D G F H C R
 361/121
 CAG CAC CAC GAC GAT TAC GAG GAC GAA ATC CGC ATG ATG TCC ACT GGC TCA AAG AAA TCC
 Q H H D D Y E D E I R M M S T G S K K S
 421/141
 CTT TTG AGC CAC GAA TTC CAG GAT GAA ACA GAC ACT GAA GAA (SEQ ID NO:65)
 L L S H E F Q D E T D T E E (SEQ ID NO:66)

FIG. 19

HBV (SEQ ID NO:67)
 DHBV (SEQ ID NO:68)

71	HBV	H	G	I	L	G	W	S	P	Q	A	Q	G	I	L	T	T	V	S	T	I	P	P	P	A	S	T	N	R	Q	S	G	R	Q	P	T	P	I	S	P	P	L	R	D	S	H	P	Q	118
69	DHBV	A	G	R	R	V	G	L	S	N	P	T	P	Q	E	I	P	Q	P	Q	W	T	P	E	E	D	Q	K	A	R	E	A	F	R	R	Y	Q	E	E	R	P	P	E	T	T	I	P	P	116

HBV (SEQ ID NO:67)	-----
DHBV (SEQ ID NO:68)	p170 binding site

FIG. 20

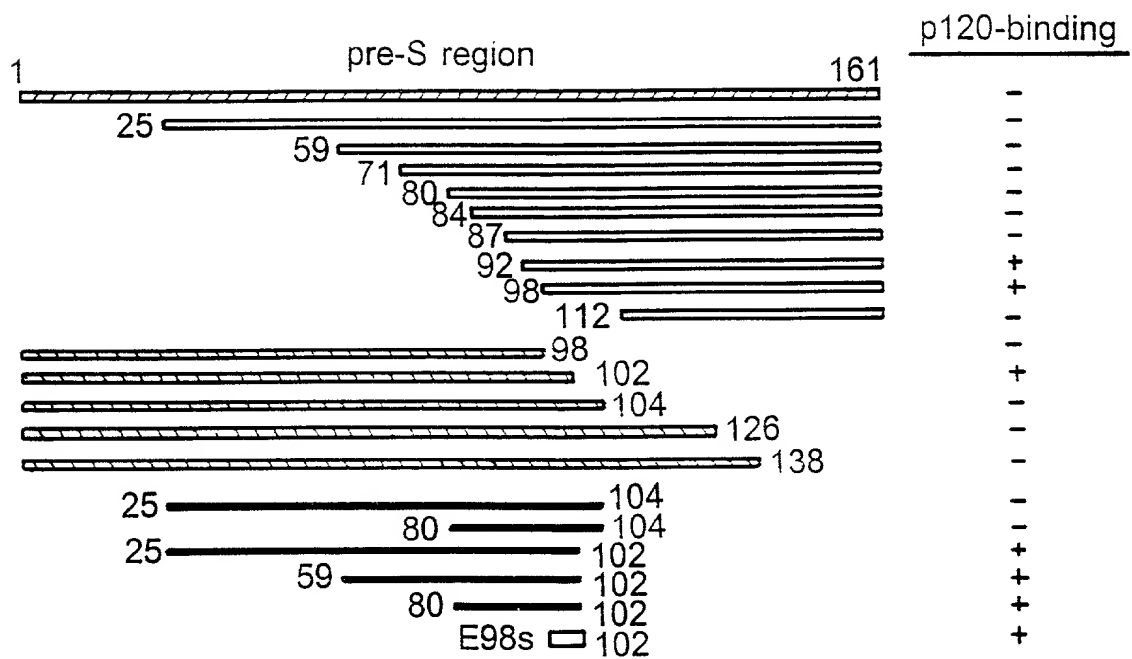


FIG. 21A

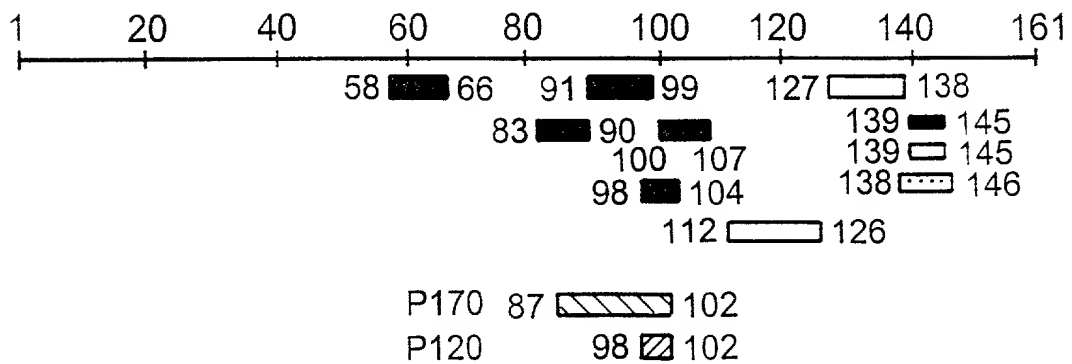


FIG. 22

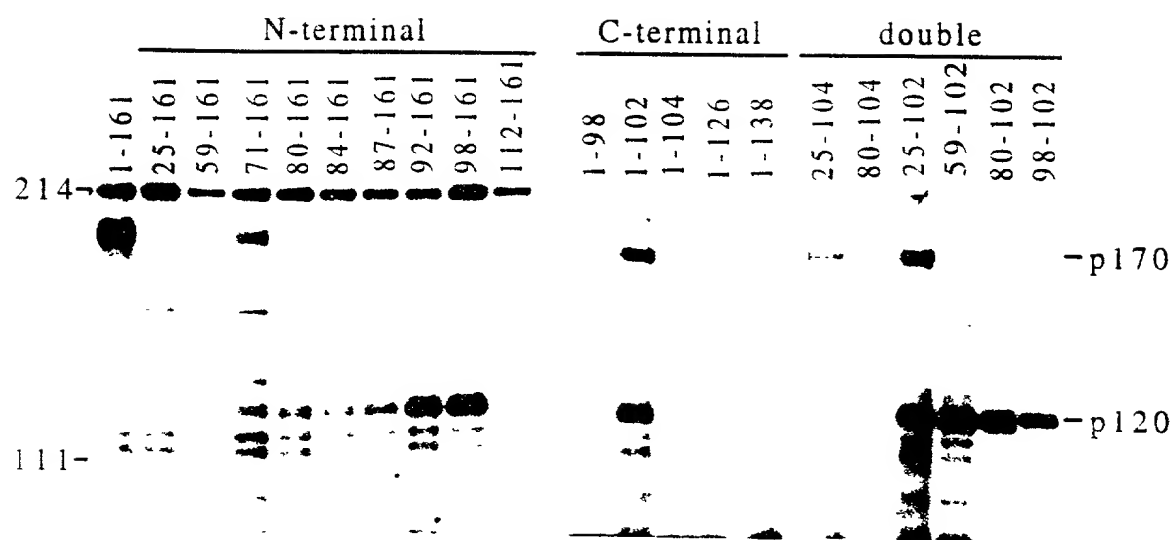


FIG. 21B

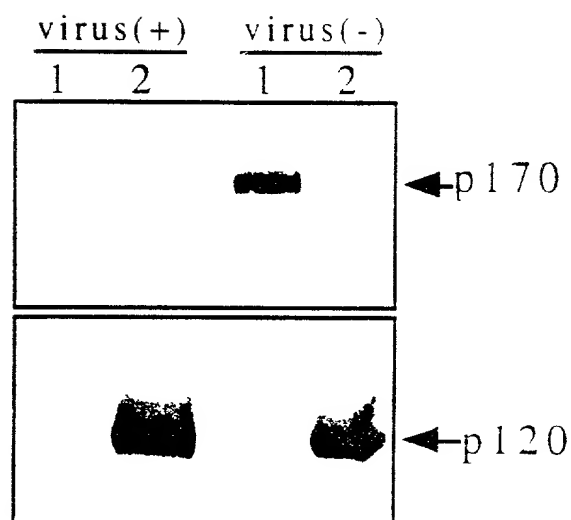


FIG. 23

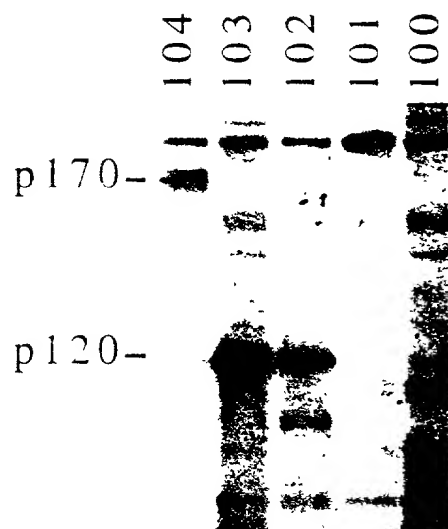


FIG. 24

			97	98	99	100	101	102	<u>p120-binding</u>
WT	Lys	Ala	Arg	Glu	Ala (Tyr)	Phe	Arg	Arg	+
R97C			Cys						+
E98V				Val					+
E98A				Ala					+
A99D					Asp				+
F100V						Val			-
F100L						Leu			-
F100W						Trp			+
R101L							Leu		-
R101H							His		-
R101K							Lys		+ weak
R102G								Gly	-
R102H								His	-
R102K								Lys	-

FIG. 25A

peptide 1: DVSGVLFQYPDTEGK (SEQ ID NO:70)

peptide 2: EVYRLALQTREQHIRRD (SEQ ID NO:71)

peptide 3: SGAQGEYAGLAAIK (SEQ ID NO:72)

peptide 4: IQPIEVDK (SEQ ID NO:73)

Peptide sequences of p120.

FIG. 30

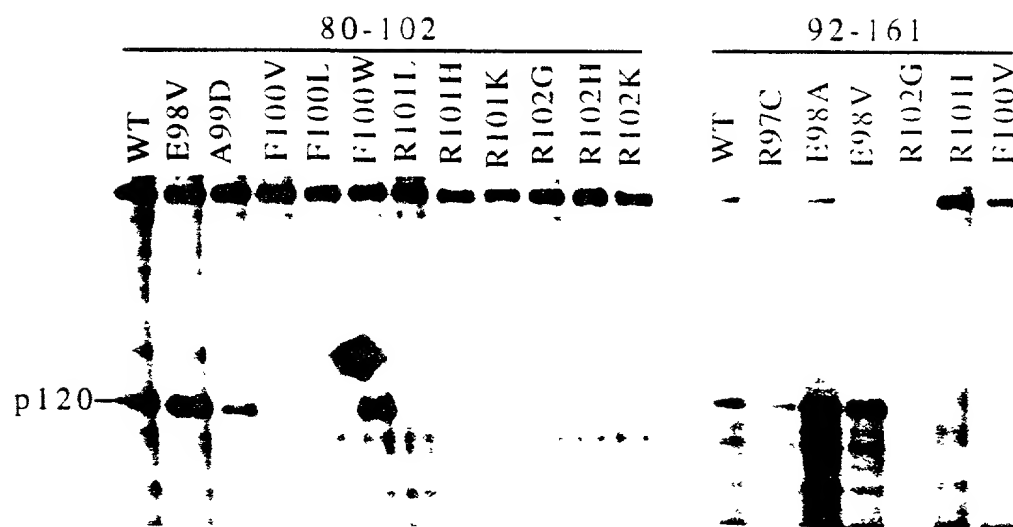


FIG. 25B

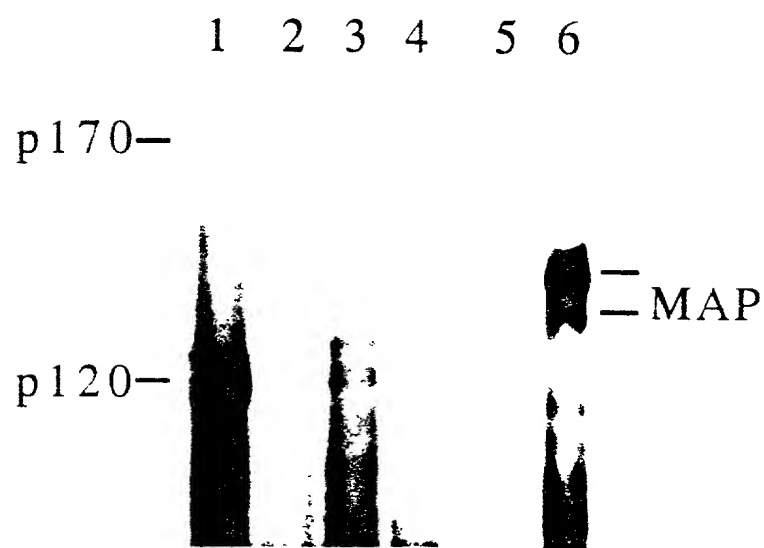


FIG. 26

1 2 3 4 5 6

FIG. 27A



FIG. 27B



FIG. 27C



FIG. 27D



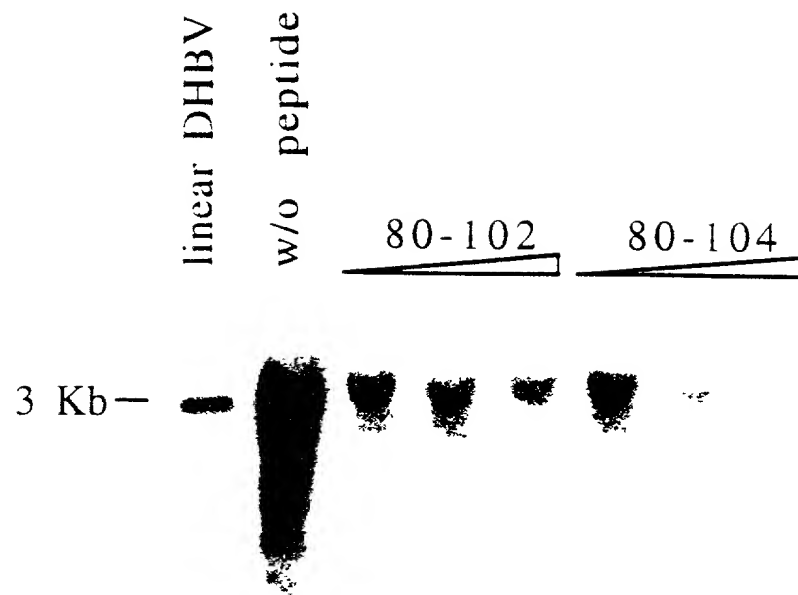


FIG. 28

A

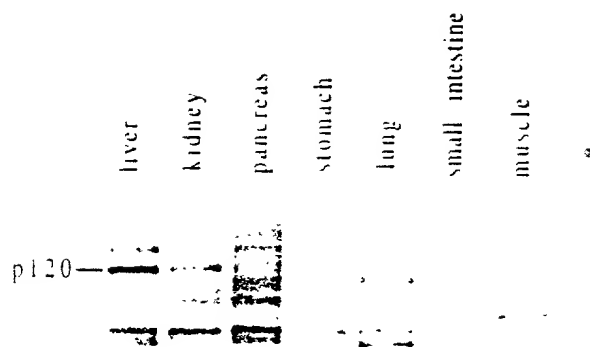


FIG. 29A

B

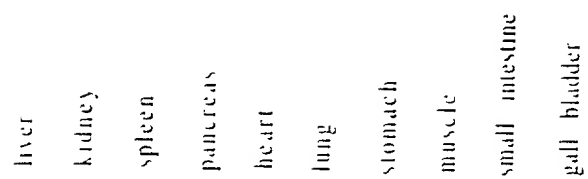


FIG. 29B

1/1
 31/11
 GAG GCG GCG CGG TGC ATC GAG CAG CTG CTG CCG CGG CAC GAT GAC TTC TCC CGG CGG CAC
 E A A R C I E Q L L P R H D D F S R R H
 61/21
 91/31
 ATC GGC CCC CGG GAG GGG GAG AAG AGG GAG ATG CTG CGA GCC CTC GGG GTG CAG AGC GTC
 I G P R E G E K R E M L R A L G V Q S V
 121/41
 151/51
 GAG GAG CTG ATG GAT AAA GCC ATC CCG GGC AGC ATC CGG CTG CGC AGG CGG CTG AGG ATG
 E E L M D K A I P G S I R L R P L R M
 181/61
 211/71
 GAG GAC CCC CTG GGT GAA AAT GAA ATC CTT GAA ACT TTA TAC AAT AAT GCA AGC AAG AAC
 E D P V G E N E I L E T L Y N I A S K N
 241/81
 271/91
 AAG ATA TGG AGG TCC TAT ATA GGC ATG GGT TAT TAC AAC TGC TCA GTG CCT CAA CCC ATT
 K I W R S Y I G M G Y Y N C S V P Q I
 301/101
 331/111
 GCA CGG AAT TTG TTG GAG AAT GCA GGA TGG GTT ACC CAG TAT ACT CCC TAC CAA CCT GAG
 A R N L L E N A G W V T Q Y T P Y Q P E
 361/121
 391/131
 GTC TCA CAG GGC AGG CTG GAG AGC CTG CTA AAT TAC CAG ACT ATG GTG TGT GAT ATC ACA
 V S Q G R L E S L L N Y Q T M V C D I T
 421/141
 451/151
 GGA ATG GAT GTG GCT AAT GCA TCA TTG CTG GAT GAG GGG ACA GCT GCT GCA GAA GCT ATG
 G M D V A N A S L L D E G T A A A E A M
 481/161
 511/171
 CAA TTA TGT CAC AGG CAC AAC AAA AGG AGG AAG TTT TAT GTA GAT TCC CGA TGC CAC CCT
 Q L C H R H N K R R K F Y V D S R C H P

FIG. 31A

541/181
CAG ACT ATA GCA GTG GTC CAA ACT AGA GCC AAT TAT ACA GGT GTT ATT ACT GAG CTC AAA
Q T I A V V Q T R A N Y T G V I T E L K
601/201
TTA CCC CAT GAG ATG GAT TTC AGT GGA AAG GAT GTC AGT GGA GTA TTA TTT CAG TAT CCA
L P H E M D F S G K D V S G V L F Q Y P
661/221
GAC ACT GAG GGG AAG GTG GAA GAC TTC TCT GAA CTT GTT GAA AGA GCT CAT CAG AAC GGG
D T E G K V E D F S E L V E R A H Q N G
721/241
ACT CTT GCC TGC TGT GCT ACT GAT CTT CTG GCT CTC TGT ATT CTG AAG CCT CCT GGA GAG
T L A C C A T D L L A L C I L K P P G E
781/261
TTT GGG GTA GAT GTT GTC CTG GGT AGC TCC CAG AGA TTT GGT GTG CCA CTC TGC TAT GGG
F G V D V V L G S S Q R F G V P L C Y G
841/281
GGA CCC CAC GCA GCA TTC TTC GCT GTC AAG GAA AAC CTA GTG AGA ATG ATG CCA GGC AGG
G P H A A F F A V K E N L V R M M P G R
901/301
ATG GTG GGT GTC ACA AGA GAT GCA AAT GGA AAA GAA GTT TAC CGA CTG GCT TTA CAA ACA
M V G V T R D A N G K E V Y R L A L Q T

FIG. 31B

961/321
 CGA GAG CAG CAT ATC AGG AGG GAC AAA GCT ACA AGC AAC ATC TGC ACA GCA CAG GCT CTT
 R E Q H I R R D K A T S N I C T A Q A L
 1021/341
 CTG GCT AAT ATG GCA GCC ATG TTT GGT GTC TAC CAT GGG TCT GAT GGA TTA AGG GAT ATT
 L A N M A A M F G V Y H G S D G L R D I
 1081/361
 GCA AGA CCG GTA CAC AAT GCT ACT TTA ATC CTG GCT GAA GGT CTC AGG AGA GCT GGT CAT
 A R R V H N A T L I L A E G L R R A G H
 1141/381
 AAA CTG CAC CAT GAT CTG TTC TTT GAT ACC TTG ACA GTC ACG TGT GGA TGC TCA GTC AAA
 K L H H D L F F D T L T V T C G C S V K
 1201/401
 GAA GTT TTG GAC AGG GCA GCT CTT AGA AAG ATA AAT TTT CGC ATT TAT AGT GAT GCC AGA
 E V L D R A A L R K I N F R I Y S D G R
 1261/421
 CTT CGA GTA TCA CTT GAT GAA ACT GTA AGT GAG AAA GAC CTA GAT GAC ATA TTA TGG ATT
 L G V S L D E T V S E K D L D D I L W I
 1321/441
 TTT GGT TGC GAG TCT TCA GCT GAA CTA ATT GCT GAA GGT ATG GGC GAG GAA ACC AAA GGT
 F G C E S S A E L I A E G M G E E T K G
 1381/461
 ATC CTT AGC ACC CCA TTT AAG AGA ACT TCC AAA TTC TTG ACC CAT CAG GTT TTC AAC AGC
 I L S T P F K R T S K F L T H Q V F N S

FIG. 31C

1441/481
 TAT CAC TCC GAA ACA AAT ATC GTA CGG TAC ATG AAG AGA TTA GAA AAC AAA GAT ATT TCC
 Y H S E T N I V R Y M K R L E N K D I S
 1501/501
 CTT GTT CAC AGC ATG ATT CCT TTG GGG TCC TGT ACA ATG AAG CTC AAT AGT TCA GCT GAA
 L V H S M I P L G S C T M K L N S S A E
 1561/521
 CTT GCA CCT ATT TCA TGG AAG GAA TTT GCC AAC ATC CAC CCC TTT GTG CCC TTG GAT CAA
 L A P I S W K E F A N I H P F V P L D Q
 1621/541
 GCT CAA GGG TAT CAG CAG CTT TTC AAG GAC TTA GAG AAG GAC CTG TGT GAG ATT ACT GGT
 A Q G Y Q Q L F K D L E K D L C E I T G
 1681/561
 TAC GAC AAA ATC TCC TTC CAA CCA AAC AGT GGA GCC CAA GGA GAG TAC GCA GGC TTG GCC
 Y D K I S F Q P N S G A Q G E Y A G L A
 1741/581
 GCA ATC AAA GCT TAT TTA AAT GCA AAA GGA GAA CGT CAT CGA AGT GTT TGC CTT ATT CCT
 A I K A Y L N A K G E R H R S V C L I P
 1801/601
 AGA TCT GCT CAT GGT ACA AAT CCA GCA AGT GCA CAG ATG GCA GGG ATG AAG ATT CAA CCA
 R S A H G T N P A S A Q M A G M K I Q P

FIG. 31D

1861/621
GTT GAA GTA GAT AAA AAT GGG AGC ATT GAT ATC TCC CAT TTA AAA GCA ATG GTG GAC AAA
V E V D K N G S I D I S H L K A M V D K

1921/641
CAC AAG GAG AAC CTG GCA GCC ATC ATG ATC ACA TAC CCT TCC ACC AAT GGT GTG TTT GAG
H K E N L A A I M I T Y P S T N G V F E

1891/631
1951/651
2011/671
GAG GAG ATT GGG GAT GTG TGT GAG CTG ATT CAC AAA AAC GGA GGC CAG GTT TAC CTG GAT
E E I G D V C E L I H K N G G Q V Y L D

2041/681
2071/691
GGA GCA AAC ATG AAC GCC CAA GTG GGT CTG TGT CGT CCT GGA GAT TAT GGC TCT GAT GTC
G A N M N A Q V G L C R P G D Y G S D V

2101/701
2131/711
TCT CAC TTA AAC CTT CAC AAA ACC TTT TGC ATT CCC CAT GGA GGA GGA CCT GGA ATG
S H L N L H K T F C I P H G G G G P G M

2161/721
2191/731
GGA CCA ATT GGA GTG AAG AAA CAT CTG GCT CCC TAC TTG CCT ACC CAT CCT GTC ATC AAG
G P I G V K K H L A P Y L P T H P V I K

FIG. 31E

2221/741
ATT CAG ACG GAT AAG GAT GCA TGT CCT TTG GGT ACT GTC AGT GCT GCA CCT TGG GGT TCC
I Q T D K D A C P L G T V S A A P W G S

2281/761
AGT GCT ATA TTG CCT ATT TCC TGG GTG TAT ATC AAG ACA ATG GGA GCA AAG GGT CTT AAA
S A I L P I S W V Y I K T M G A K G L K

2341/781
CAC GCT TCT GAG GTT GCT ATA TTA AAT GCA AAC TAC ATG GCA AAG AGG CTG GAG AAG CAC
H A S E V A I L N A N Y M A K R L E K H

2401/801
TAC AAA ATC CTT TTC AGA GGA GTA AGA GGT TAT GTA GCC CAT GAA TTC ATT TTG GAT ACA
Y K I L F R G V R G Y V A H E F I L D T

2461/821
AGA CCT TTC AAA ACA GCA AAC ATT GAA GCT GTG GAT CTT GCT AAG CGA CTT CAG GAT
R P F K K T A N I E A V D L A K R L Q D

2521/841
TAT GGT TTT CAT GCT CCA ACC ATG TCC TGG CCA GTG GCA GGC ACA CTT ATG ATT GAA CCA
Y G F H A P T M S W P V A G T L M I E P

2581/861
ACA GAG TCT GAA GAC AAG GCA GAG CTG GAC ACG TTT TGT GAT GCA ATG ATC AGT ATT CGA
T E S E D K A E L D R F C D A M I S I R

2251/751
2311/771
2371/791
2431/811
2491/831
2551/851
2611/871

FIG. 31F

2641/881
CAG GAA ATT GCT GAA ATA GAG GAG GGC AGG ATG GAC CCT CAG ATT AAC CCA TTA AAG ATG
Q E I A E I E E G R M D P Q I N P L K M
2701/901
TCA CCA CAT ACT CTA AAC TGT GTC ACT TCT TCA AAG TGG GAT CGT CCT TAT TCC AGA GAA
S P H T L N C V T S S K W D R P Y S R E
2761/921
GTG GCA GCA TTC CCA CTG CCG TTT GTG AAA CCT GAG AGC AAG TTT TGG CCC ACA ATT GCT
V A A F P L P F V K P E S K F W P T I A
2821/941
CGC ATC GAT GAC ATA TAC GGA GAT CAA CAC CTG GTT TGT ACC TGC CCA CCG ATG GAA GCC
R I D D I Y G D Q H L V C T C P P M E A
2881/961
TAC GAA TCT CCC TTC TCT GAA CAG AAG AGA GCA TCT TCG TAA (SEQ ID NO:74)
Y E S P F S E Q K R A S S * (SEQ ID NO:75)

FIG. 31G